



#3

SUBSTITUTE SEQUENCE LISTING

<110> Lima, Christopher
Mossesso, Elena

<120> Structure-Based Drug Design for Ulp1 Protease Substrates

<130> 2650/1G681-US1

<140> 09/856,247

<141> 2001-05-17

<150> 60/205,336

<151> 2000-05-18

<160> 2

<170> PatentIn version 3.0

<210> 1

<211> 1866

<212> DNA

<213> *Saccharomyces cerevisiae*

<400> 1

```
atgtcagttg aagtagataa gcaccggaac acactacagt atcataaaaa gaacccttac      60
tcccccttat tctccccaat ttctacatat aggtgttata ctcgggtatt gaacaatccc      120
tcgagtgcta gaagatcagc cagtttttagt ggtatttata aaaaaagaac caatacgtca      180
agattcaatt atttaaacga ccgcctgtgtt ttatcaatgg aagaatcaat gaaagatggg      240
tcagatagag ctagtaaagc tggttttata ggaggcataa gagaaactct ttggaactca      300
ggtaagtact tatggcacac atttgtgaaa aacgaacctc gcaattttga tggttctgaa      360
gtagaagcaa gtggtaacag cgacgttgag agcagaagtt ctggaagtag gagcagtgac      420
gtaccatatg gtctacgtga aaattattcc tcggatacaa gaaaacacaa attcgatagc      480
tcgacgtggg ccttaccaaa taaaaggaga agaatcgaaa gtgaagggtg ggggacacct      540
tcaacctcac caatcagctc tttggcttct caaaaaagca attgtgatag tgacaatagc      600
ataacttttt cgagagatcc ttttggttgg aataagtgga aaacaagtg c tattggttct      660
aactcagaaa ataacacttc tgatcagaaa aatagctacg acaggcgaca gtatgggaca      720
gcctttatta gaaagaaaaa agttgcaaaa cagaacatta acaatactaa actggtgtcg      780
agagcacaat ctgaggaagt aacatattta cgacaaatat tcaacggaga atataaagtt      840
ccaaaaatat taaaagaaga aagagaaaga cagttaaaat taatggatat ggataaggaa      900
aaagacactg gcttaaaaaa gtctataatc gacttaactg aaaagatcaa aacaatttta      960
attgagaaca acaagaacag actacagaca agaaatgaaa atgatgatga tttagtattt     1020
gttaaagaaa aaaagatatc ttctttggaa aggaaacata aggattactt aaatcaaaag     1080
```

```

ttgaagtttg atagatctat attagagttt gagaaagact tcaaaagata taacgaaatt 1140
ttaaataaaa gaaagaagat tcaagaagat cttaaaaaaa agaaagaaca attggccaag 1200
aagaaacttg ttcctgaatt aaatgaaaaa gacgatgacc aagtacaaaa agctttggca 1260
tctagagaaa atactcagtt aatgaataga gataatatag agataacagt acgtgatttt 1320
aagaccttgg caccacgaag atggctaaat gacactatca ttgagttttt tatgaaatac 1380
attgaaaaat ctaccctaa tacagtggcg ttttaattcat ttttctatac caatttatca 1440
gaaaggggtt atcaaggcgt ccggagggtg atgaagagaa agaagacaca aattgataaa 1500
cttgataaaa tctttacacc aataaatttg aaccaatccc actgggcgtt gggcataatt 1560
gatttaaaaa agaaaactat aggttacgta gattcattat cgaatgggcc aaatgctatg 1620
agtttcgcta tactgactga cttgcaaaaa tatgttatgg aggaaagtaa gcatacaata 1680
ggagaagact ttgatttgat tcatttagat tgtccgcagc aaccaaattg ctacgactgt 1740
ggaatatatg tttgtatgaa tactctctat ggaagtgcag atgcgccatt ggattttgat 1800
tataaagatg cgattagatg gagaagattt attgcccatt tgattttaac cgacgcttta 1860
aaatag 1866

```

```

<210> 2
<211> 621
<212> PRT
<213> Saccharomyces cerevisiae

```

<400> 2

```

Met Ser Val Glu Val Asp Lys His Arg Asn Thr Leu Gln Tyr His Lys
1           5           10           15
Lys Asn Pro Tyr Ser Pro Leu Phe Ser Pro Ile Ser Thr Tyr Arg Cys
20          25          30
Tyr Pro Arg Val Leu Asn Asn Pro Ser Glu Ser Arg Arg Ser Ala Ser
35          40          45
Phe Ser Gly Ile Tyr Lys Lys Arg Thr Asn Thr Ser Arg Phe Asn Tyr
50          55          60
Leu Asn Asp Arg Arg Val Leu Ser Met Glu Glu Ser Met Lys Asp Gly
65          70          75          80
Ser Asp Arg Ala Ser Lys Ala Gly Phe Ile Gly Gly Ile Arg Glu Thr
85          90          95
Leu Trp Asn Ser Gly Lys Tyr Leu Trp His Thr Phe Val Lys Asn Glu
100         105         110
Pro Arg Asn Phe Asp Gly Ser Glu Val Glu Ala Ser Gly Asn Ser Asp
115         120         125

```

Val Glu Ser Arg Ser Ser Gly Ser Arg Ser Ser Asp Val Pro Tyr Gly
130 135 140
Leu Arg Glu Asn Tyr Ser Ser Asp Thr Arg Lys His Lys Phe Asp Thr
145 150 155 160
Ser Thr Trp Ala Leu Pro Asn Lys Arg Arg Arg Ile Glu Ser Glu Gly
165 170 175
Val Gly Thr Pro Ser Thr Ser Pro Ile Ser Ser Leu Ala Ser Gln Lys
180 185 190
Ser Asn Cys Asp Ser Asp Asn Ser Ile Thr Phe Ser Arg Asp Pro Phe
195 200 205
Gly Trp Asn Lys Trp Lys Thr Ser Ala Ile Gly Ser Asn Ser Glu Asn
210 215 220
Asn Thr Ser Asp Gln Lys Asn Ser Tyr Asp Arg Arg Gln Tyr Gly Thr
225 230 235 240
Ala Phe Ile Arg Lys Lys Lys Val Ala Lys Gln Asn Ile Asn Asn Thr
245 250 255
Lys Leu Val Ser Arg Ala Gln Ser Glu Glu Val Thr Tyr Leu Arg Gln
260 265 270
Ile Phe Asn Gly Glu Tyr Lys Val Pro Lys Ile Leu Lys Glu Glu Arg
275 280 285
Glu Arg Gln Leu Lys Leu Met Asp Met Asp Lys Glu Lys Asp Thr Gly
290 295 300
Leu Lys Lys Ser Ile Ile Asp Leu Thr Glu Lys Ile Lys Thr Ile Leu
305 310 315 320
Ile Glu Asn Asn Lys Asn Arg Leu Gln Thr Arg Asn Glu Asn Asp Asp
325 330 335
Asp Leu Val Phe Val Lys Glu Lys Lys Ile Ser Ser Leu Glu Arg Lys
340 345 350
His Lys Asp Tyr Leu Asn Gln Lys Leu Lys Phe Asp Arg Ser Ile Leu
355 360 365
Glu Phe Glu Lys Asp Phe Lys Arg Tyr Asn Glu Ile Leu Asn Glu Arg
370 375 380
Lys Lys Ile Gln Glu Asp Leu Lys Lys Lys Lys Glu Gln Leu Ala Lys
385 390 395 400
Lys Lys Leu Val Pro Glu Leu Asn Glu Lys Asp Asp Asp Gln Val Gln
405 410 415
Lys Ala Leu Ala Ser Arg Glu Asn Thr Gln Leu Met Asn Arg Asp Asn
420 425 430
Ile Glu Ile Thr Val Arg Asp Phe Lys Thr Leu Ala Pro Arg Arg Trp
435 440 445

Leu Asn Asp Thr Ile Ile Glu Phe Phe Met Lys Tyr Ile Glu Lys Ser
 450 455 460
 Thr Pro Asn Thr Val Ala Phe Asn Ser Phe Phe Tyr Thr Asn Leu Ser
 465 470 475 480
 Glu Arg Gly Tyr Gln Gly Val Arg Arg Trp Met Lys Arg Lys Lys Thr
 485 490 495
 Gln Ile Asp Lys Leu Asp Lys Ile Phe Thr Pro Ile Asn Leu Asn Gln
 500 505 510
 Ser His Trp Ala Leu Gly Ile Ile Asp Leu Lys Lys Lys Thr Ile Gly
 515 520 525
 Tyr Val Asp Ser Leu Ser Asn Gly Pro Asn Ala Met Ser Phe Ala Ile
 530 535 540
 Leu Thr Asp Leu Gln Lys Tyr Val Met Glu Glu Ser Lys His Thr Ile
 545 550 555 560
 Gly Glu Asp Phe Asp Leu Ile His Leu Asp Cys Pro Gln Gln Pro Asn
 565 570 575
 Gly Tyr Asp Cys Gly Ile Tyr Val Cys Met Asn Thr Leu Tyr Gly Ser
 580 585 590
 Ala Asp Ala Pro Leu Asp Phe Asp Tyr Lys Asp Ala Ile Arg Met Arg
 595 600 605
 Arg Phe Ile Ala His Leu Ile Leu Thr Asp Ala Leu Lys
 610 615 620